Enhancers: Multi-dimensional signal integrators.

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Public Summary:
A lot of human genes are only expressed in certain tissues, and such tissue-specific pattern is controlled by certain small DNA-sequences called enhancers. It has been discovered that in human genome, enhancers are associated with certain proteins and/or RNA product. These knowledge has allowed the identification of enhancers in a genome scale with the help of modern genomic technologies. On the other hand, although tissue-specific gene expression has been found to be highly correlated with tissue specific enhancer activity, the molecular mechanisms of such correlation have not been fully characterized. Based on recent literature and our own work, this point-of-view article proposes a model in which enhancers function as a central platform integrating all the inputs, including information from both within the cell and outside the cells, and producing highly specific gene expression programs.

Scientific Abstract:
Enhancers play a critical role in regulating tissue-specific gene expression, but their molecular mechanisms of function have not been fully characterized. It is now increasingly clear that enhancers associate with specific protein factors and chromatin modifications and also produce non-coding RNAs known as eRNAs. These predictive signatures have facilitated genomic identification of enhancers and helped characterize tissue-specific gene expression mechanisms. Herein we review recent studies investigating enhancers in mammalian cells, and propose that enhancers function as a central platform integrating lineage-specific transcription factors and epigenetic states with ubiquitous yet signal-dependent transcriptional inputs, culminating in highly specific gene expression programs.